

SEQUENCE LISTING

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<120> ANTIBODIES AGAINST LESIONAL TISSUES

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tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg	144
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
35 40 45	
gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt	192
Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe	
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Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr	
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atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt	288
Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa 336
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 35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
 50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
 65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
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 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
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 35 40 45
 gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
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 aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
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 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg 336
 Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp
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 35 40 45
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
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 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
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 35 40 45
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 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
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 65 70 75 80
 ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg 336
 Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp
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 35 40 45
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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 aca gtg aca atc tcc tgc aag gtt tct gga cac aac ttc atc gac cac 96
 Thr Val Thr Ile Ser Cys Lys Val Ser Gly His Asn Phe Ile Asp His
 20 25 30
 tac atg cat tgg gta caa cag gcc cct gga aaa ggg ctt gac tgg atg 144
 Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Asp Trp Met
 35 40 45
 gga cta att gac cct gaa gat ggt cag acg aaa tat tca gag agg ttt 192
 Gly Leu Ile Asp Pro Glu Asp Gly Gln Thr Lys Tyr Ser Glu Arg Phe
 50 55 60
 gag ggc aga gtc aca att acc gcg gac aag tca aca gac aca acc tac 240
 Glu Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asp Thr Thr Tyr
 65 70 75 80
 ttg gag gtg agc ggc ctg aga tcg gaa gac acg gcc gtt tat ttc tgt 288
 Leu Glu Val Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95
 aca acg gac ttg ggt gac ttg aat tat tgg aac cct ggt cac cgt ctc 336
 Thr Thr Asp Leu Gly Asp Leu Asn Tyr Trp Asn Pro Gly His Arg Leu

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Leu

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35 40 45
Gly Leu Ile Asp Pro Glu Asp Gly Gln Thr Lys Tyr Ser Glu Arg Phe
50 55 60
Glu Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asp Thr Thr Tyr
65 70 75 80
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85 90 95
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Leu

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tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
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 tct ctg aag atc tcc tgt cag ggt tct gga tac aca ttt agc aat tac 96
 Ser Leu Lys Ile Ser Cys Gln Gly Ser Gly Tyr Thr Phe Ser Asn Tyr
 20 25 30
 tgg atc gcc tgg gtg cgc cag agg ccc ggg aaa ggc ctg gag tgg atg 144
 Trp Ile Ala Trp Val Arg Gln Arg Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 ggg atc atc tat cct ggt gac tct gat atc aaa tac agt ccg tcc ttc 192
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ile Lys Tyr Ser Pro Ser Phe
 50 55 60
 caa ggc cat gtc acc atc tca gcc gac acg tcc atg aac acc gcc tac 240
 Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Met Asn Thr Ala Tyr
 65 70 75 80
 ctg cag tgg aac acc ctg aag gcc tcg gac acc gcc atg tac tac tgt 288
 Leu Gln Trp Asn Thr Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 gcg aga cat aaa ggg acc agg ttc ggg gag gtt ttg gcg gtt ggc aac 336
 Ala Arg His Lys Gly Thr Arg Phe Gly Glu Val Leu Ala Val Gly Asn
 100 105 110
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 Trp Ile Ala Trp Val Arg Gln Arg Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ile Lys Tyr Ser Pro Ser Phe
 50 55 60

Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Met Asn Thr Ala Tyr
 65 70 75 80

Leu Gln Trp Asn Thr Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg His Lys Gly Thr Arg Phe Gly Glu Val Leu Ala Val Gly Asn
 100 105 110

Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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 Ser Val Lys Phe Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Asn Tyr
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 gct atc acc tgg gtg cga cag gcc cct gga caa ggt ctt gag tgg atg 144
 Ala Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 gga agg atc atc cct atc ttt ggt ata cca aac tac gca cag gaa ttc 192
 Gly Arg Ile Ile Pro Ile Phe Gly Ile Pro Asn Tyr Ala Gln Glu Phe
 50 55 60
 cag ggc aga gtc acg att acc gcc gac gat tcc acg acc aca gtc tac 240
 Gln Gly Arg Val Thr Ile Thr Ala Asp Asp Ser Thr Thr Thr Val Tyr
 65 70 75 80
 atg gaa ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt 288
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gat aat tca ata gga gca cct gat act tgg tgg ttc gac ccc 336
 Ala Arg Asp Asn Ser Ile Gly Ala Pro Asp Thr Trp Trp Phe Asp Pro
 100 105 110
 tgg ggc cag gga cca cgg tca ccg tct cct ca 368

Trp Gly Gln Gly Pro Arg Ser Pro Ser Pro
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 35 40 45
 Gly Arg Ile Ile Pro Ile Phe Gly Ile Pro Asn Tyr Ala Gln Glu Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Asp Ser Thr Thr Thr Val Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Asn Ser Ile Gly Ala Pro Asp Thr Trp Trp Phe Asp Pro
 100 105 110
 Trp Gly Gln Gly Pro Arg Ser Pro Ser Pro
 115 120

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 <222> (1)..(360)
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 Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
 20 25 30
 tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt 192
 Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
 50 55 60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac 240
 Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
 65 70 75 80

atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt 288
 Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa 336
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 35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
 50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
 65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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 100 105 110

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<222> (1)..(363)

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tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttc	agt	agc	aat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Asn	
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Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
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Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	
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65					70				75					80		

ctg	caa	atg	aac	agc	ctg	agg	gcc	gag	gac	acg	gct	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		

gcg	aga	gat	cac	ggc	ctt	ggt	gat	caa	gcc	tcc	tgg	ttc	gac	ccc	tgg	336
Ala	Arg	Asp	His	Gly	Leu	Gly	Asp	Gln	Ala	Ser	Trp	Phe	Asp	Pro	Trp	
			100					105					110			

ggc	cag	gga	acc	ctg	gtc	acc	gtc	tcc	tc							365
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser								
		115					120									

<210> 18

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<212> PRT

<213> Homo sapiens

<400> 18

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
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			20					25					30			

Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				

Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	
	50					55					60					

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser
115 120

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tcc ctg aga ctc tcc tgt gca gcc tct gga ttc agc ttc agt agc tat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gca gtt ata tgg tat gat gga agc tat aaa tac tat gca gaa tcc gtg 192
Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val
50 55 60

aag ggc cga ttc atc atc tcc aga gac aat tcc aag aac acc ctg tat 240
Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtc tat tac tgt 288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga gat cgg ggg tcg gtg gag atg gct aca atc gcg gac tac tgg 336
Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp
100 105 110

ggc cag gga acc ctg gtc acc gtc tcc tca 366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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 <213> Homo sapiens

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 35 40 45
 Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val
 50 55 60
 Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gca gtt ata tgg tat gat gga agt tat aaa tac tat gca gaa tcc gtg 192
 Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val

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aag ggc cga ttc atc atc tcc aga gac aat tcc aag aac acc ctg tat			240
Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt			288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
	85	90	95
gcg aga gat cgg ggg tcg gta gag atg gct aca atc gcg gac tac tgg			336
Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp			
	100	105	110
ggc cag gga acc ctg gtc acc gtc tcc tca			366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser			
	115	120	

<210> 22
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 <213> Homo sapiens

<400> 22	
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg	
1	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr	
	30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
	45
Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val	
	60
Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
	95
Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp	
	110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
	120

<210> 23
 <211> 366
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (1) .. (366)

<223>

<400> 23

cag	gtc	cag	ctg	gtg	caa	tct	ggg	gga	ggc	gtg	gtc	cag	cct	ggg	agg	48
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1				5					10					15		

tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	agc	ttc	agt	agc	tat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Ser	Ser	Tyr	
			20					25					30			

ggc	atg	cac	tgg	gtc	cgc	cag	gct	cca	ggc	aag	ggg	ctg	gag	tgg	gtg	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				

gca	gtt	ata	tgg	tat	gat	gga	agt	tat	aaa	tac	tat	gca	gaa	tcc	gtg	192
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Tyr	Lys	Tyr	Tyr	Ala	Glu	Ser	Val	
	50					55					60					

aag	ggc	cga	ttc	atc	atc	tcc	aga	gac	aat	tcc	aag	aac	acc	ctg	tat	240
Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65				70					75					80		

ctg	caa	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gct	gtc	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			

gcg	aga	gat	cgg	ggg	tcg	gta	gag	atg	gct	aca	atc	gcg	gac	tac	tgg	336
Ala	Arg	Asp	Arg	Gly	Ser	Val	Glu	Met	Ala	Thr	Ile	Ala	Asp	Tyr	Trp	
			100				105					110				

ggc	cag	gga	acc	ctg	gtc	acc	gtc	tcc	tca							366
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
		115					120									

<210> 24

<211> 122

<212> PRT

<213> Homo sapiens

<400> 24

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5					10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Ser	Ser	Tyr
			20					25					30		

Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Tyr	Lys	Tyr	Tyr	Ala	Glu	Ser	Val
	50					55					60				

Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65				70					75					80	

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 25
 <211> 370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(369)
 <223>

<400> 25
 cag gta cag ctg cag cag tca ggt cca gga ctg gtg aag ccc tcg cag 48
 Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15

acc ctc tca ctc acc tgt gcc atc tcc ggg gac agt gtc tct agc aac 96
 Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
 20 25 30

agt gct gct tgg cac tgg atc agg cag tcc cca tcg aga ggc ctt gag 144
 Ser Ala Ala Trp His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
 35 40 45

tgg ctg gga agg aca tac tac agg tcc aag tgg tat aat gat tat aca 192
 Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Thr
 50 55 60

gtg tct gtg aaa agt cga ata acc atc aag cca gac aca tcc aag aac 240
 Val Ser Val Lys Ser Arg Ile Thr Ile Lys Pro Asp Thr Ser Lys Asn
 65 70 75 80

cag ttc tcc ctg cag ctg aac tct gtg act ccc gag gac acg gct gtg 288
 Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95

tat tac tgt gca aga tca cag gaa gag cac cgg tcg ttg gat gat gct 336
 Tyr Tyr Cys Ala Arg Ser Gln Glu His Arg Ser Leu Asp Asp Ala
 100 105 110

ttt gat atc tgg gac cac ggt cac cgt ctc ctc a 370
 Phe Asp Ile Trp Asp His Gly His Arg Leu Leu
 115 120

<210> 26
 <211> 123

<212> PRT
 <213> Homo sapiens

<400> 26

Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gln	
1				5					10					15		
Thr	Leu	Ser	Leu	Thr	Cys	Ala	Ile	Ser	Gly	Asp	Ser	Val	Ser	Ser	Asn	
			20					25					30			
Ser	Ala	Ala	Trp	His	Trp	Ile	Arg	Gln	Ser	Pro	Ser	Arg	Gly	Leu	Glu	
		35					40					45				
Trp	Leu	Gly	Arg	Thr	Tyr	Tyr	Arg	Ser	Lys	Trp	Tyr	Asn	Asp	Tyr	Thr	
	50					55					60					
Val	Ser	Val	Lys	Ser	Arg	Ile	Thr	Ile	Lys	Pro	Asp	Thr	Ser	Lys	Asn	
65					70					75					80	
Gln	Phe	Ser	Leu	Gln	Leu	Asn	Ser	Val	Thr	Pro	Glu	Asp	Thr	Ala	Val	
				85					90					95		
Tyr	Tyr	Cys	Ala	Arg	Ser	Gln	Glu	Glu	His	Arg	Ser	Leu	Asp	Asp	Ala	
			100					105					110			
Phe	Asp	Ile	Trp	Asp	His	Gly	His	Arg	Leu	Leu						
		115					120									

<210> 27
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(360)
 <223>

<400> 27

cag	gtc	cag	ctg	gtg	caa	tct	ggg	gct	gag	gtg	aag	aag	cct	ggg	gcc	48
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	
1				5				10						15		
tca	gtg	aag	gtc	tcc	tgt	cag	gct	tct	gga	tac	atg	ttc	acc	ggc	ttc	96
Ser	Val	Lys	Val	Ser	Cys	Gln	Ala	Ser	Gly	Tyr	Met	Phe	Thr	Gly	Phe	
			20					25					30			
tat	atg	cac	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggg	ctt	gag	tgg	atg	144
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		35				40					45					
gga	tgg	atg	aac	act	aac	agt	ggg	gcc	aca	ggc	tat	gca	cac	aag	ttt	192
Gly	Trp	Met	Asn	Thr	Asn	Ser	Gly	Ala	Thr	Gly	Tyr	Ala	His	Lys	Phe	
	50					55				60						
cag	gac	agg	gtc	acc	ctg	acc	agg	gac	acg	tcc	atc	agc	aca	ggc	tac	240

Gln	Asp	Arg	Val	Thr	Leu	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Gly	Tyr		
65					70					75					80		
atg	gag	ctg	ggc	ggc	ctg	aca	tct	gac	gac	acg	gcc	gtg	tat	tat	tgt		288
Met	Glu	Leu	Gly	Gly	Leu	Thr	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
			85					90					95				
gcg	aga	acc	cag	gag	gtt	tac	tac	tac	gct	atg	gac	gtc	tgg	ggc	caa		336
Ala	Arg	Thr	Gln	Glu	Val	Tyr	Tyr	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln		
			100					105					110				
ggg	aca	atg	gtc	acc	gtc	tct	tca										360
Gly	Thr	Met	Val	Thr	Val	Ser	Ser										
		115				120											

<210> 28
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400>	28																
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala		
1			5					10					15				
Ser	Val	Lys	Val	Ser	Cys	Gln	Ala	Ser	Gly	Tyr	Met	Phe	Thr	Gly	Phe		
		20				25						30					
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met		
		35				40					45						
Gly	Trp	Met	Asn	Thr	Asn	Ser	Gly	Ala	Thr	Gly	Tyr	Ala	His	Lys	Phe		
	50				55					60							
Gln	Asp	Arg	Val	Thr	Leu	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Gly	Tyr		
65					70					75					80		
Met	Glu	Leu	Gly	Gly	Leu	Thr	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
			85					90					95				
Ala	Arg	Thr	Gln	Glu	Val	Tyr	Tyr	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln		
			100					105					110				
Gly	Thr	Met	Val	Thr	Val	Ser	Ser										
		115				120											

<210> 29
 <211> 348
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (348)
 <223>

<400> 29
 cag gtc cag ctg gtg caa tct ggg gct gag gtg agg aag ccc ggg acg 48
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Thr
 1 5 10 15

 aca gtg aca atc tcc tgc aag gtt tct gga cac aac ttc atc gac cac 96
 Thr Val Thr Ile Ser Cys Lys Val Ser Gly His Asn Phe Ile Asp His
 20 25 30

 tac atg cat tgg gta caa cag gcc cct gga aaa ggg ctt gac tgg atg 144
 Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Asp Trp Met
 35 40 45

 gga cta att gac cct gaa gat ggt cag acg aaa tat tca gag agg ttt 192
 Gly Leu Ile Asp Pro Glu Asp Gly Gln Thr Lys Tyr Ser Glu Arg Phe
 50 55 60

 gag ggc aga gtc aca att acc gcg gac aag tca aca gac aca acc tac 240
 Glu Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asp Thr Thr Tyr
 65 70 75 80

 ttg gag gtg agc ggc ctg aga tcg gaa gac acg gcc gtt tat ttc tgt 288
 Leu Glu Val Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

 aca acg gac ttg ggt gac ttg aat tat tgg ggc cag gga acc ctg gtc 336
 Thr Thr Asp Leu Gly Asp Leu Asn Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

 acc gtc tcc tca 348
 Thr Val Ser Ser
 115

 <210> 30
 <211> 116
 <212> PRT
 <213> Homo sapiens

 <400> 30
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Thr
 1 5 10 15

 Thr Val Thr Ile Ser Cys Lys Val Ser Gly His Asn Phe Ile Asp His
 20 25 30

 Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Asp Trp Met
 35 40 45

 Gly Leu Ile Asp Pro Glu Asp Gly Gln Thr Lys Tyr Ser Glu Arg Phe
 50 55 60

 Glu Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asp Thr Thr Tyr
 65 70 75 80

 Leu Glu Val Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Thr Thr Asp Leu Gly Asp Leu Asn Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 31
 <211> 366
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(366)
 <223>

<400> 31
 cag gtc cag ctg gtg caa tct ggg gga ggc gtg gtc cag cct ggg agg 48
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg 336
 Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp
 100 105 110
 ggc cag ggc acc ctg gtc acc gtc tcc tca 366
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 32
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 32

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 33

<211> 368

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (366)

<223>

<400> 33

cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag tct ggg gcc 48
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Ser Gly Ala
 1 5 10 15

tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc acc ggc cac 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly His
 20 25 30

ttt atc cac tgg gtg cgg cag gcc cct gga caa ggg ctt gag tgg atg 144
 Phe Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

gga tgg atc aac cct aac gtt ggt gtc aca aat tat gca cag aag ttt 192
 Gly Trp Ile Asn Pro Asn Val Gly Val Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

cag ggc agg gtc acc atg acc agg gac acg tcc ata agc aca gcc tac 240
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

ata gaa ctg agg agg ctg aga tct gac gac acg gcc gtg tat tac tgt 288
 Ile Glu Leu Arg Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gtg aga gaa tcc gac aca gct gcg gtg gcc tac tac tac cac ggt atg 336
 Val Arg Glu Ser Asp Thr Ala Ala Val Ala Tyr Tyr Tyr His Gly Met
 100 105 110

gac gtc tgg gga caa tgg tca ccg tct ctt ca 368
 Asp Val Trp Gly Gln Trp Ser Pro Ser Leu
 115 120

<210> 34
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 34
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Ser Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly His
 20 25 30

Phe Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Val Gly Val Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Val Arg Glu Ser Asp Thr Ala Ala Val Ala Tyr Tyr Tyr His Gly Met
 100 105 110

Asp Val Trp Gly Gln Trp Ser Pro Ser Leu
 115 120

<210> 35
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(375)
 <223>

<400> 35
 cag gtc cag ctg gtg caa tct ggg gga gac tgg gta aag cct ggg ggg 48
 Gln Val Gln Leu Val Gln Ser Gly Gly Asp Trp Val Lys Pro Gly Gly

1	5	10	15	
tcc ctt aga ctc tcc tgt gca gcg tct gga ttc cct ttc gct aat gcc				96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ala Asn Ala				
	20	25	30	
tgg atg tat tgg ttc cgc cag gct cca ggg aag ggg ctg gag tgg gtt				144
Trp Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val				
	35	40	45	
ggc cgt att aaa agc aaa cca agt ggt ggg gct aca gag ttc gct gca				192
Gly Arg Ile Lys Ser Lys Pro Ser Gly Gly Ala Thr Glu Phe Ala Ala				
	50	55	60	
ccc gtg gaa ggt aga ttc agc atc tcc aga gac gat tcg aaa aac acg				240
Pro Val Glu Gly Arg Phe Ser Ile Ser Arg Asp Asp Ser Lys Asn Thr				
	65	70	75	80
atg gat ctg caa atg aat agc ctg aga acc gac gac aca gcc gta tat				288
Met Asp Leu Gln Met Asn Ser Leu Arg Thr Asp Asp Thr Ala Val Tyr				
	85	90	95	
tat tgt acc aca gat tgg ggt tcg ggg acc tat cat aag ttt gct tta				336
Tyr Cys Thr Thr Asp Trp Gly Ser Gly Thr Tyr His Lys Phe Ala Leu				
	100	105	110	
gat gtc tgg ggc caa ggg aca atg gtc acc gtc tct tca				375
Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser				
	115	120	125	
<210> 36				
<211> 125				
<212> PRT				
<213> Homo sapiens				
<400> 36				
Gln Val Gln Leu Val Gln Ser Gly Gly Asp Trp Val Lys Pro Gly Gly				
1	5	10	15	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ala Asn Ala				
	20	25	30	
Trp Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val				
	35	40	45	
Gly Arg Ile Lys Ser Lys Pro Ser Gly Gly Ala Thr Glu Phe Ala Ala				
	50	55	60	
Pro Val Glu Gly Arg Phe Ser Ile Ser Arg Asp Asp Ser Lys Asn Thr				
	65	70	75	80
Met Asp Leu Gln Met Asn Ser Leu Arg Thr Asp Asp Thr Ala Val Tyr				
	85	90	95	
Tyr Cys Thr Thr Asp Trp Gly Ser Gly Thr Tyr His Lys Phe Ala Leu				
	100	105	110	

Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120 125

<210> 37
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(357)
 <223>

<400> 37
 gtg cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc tca 48
 Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 1 5 10 15
 gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc tat 96
 Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr
 20 25 30
 atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga 144
 Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
 35 40 45
 tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt cag 192
 Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln
 50 55 60
 gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac atg 240
 Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met
 65 70 75 80
 gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt gcg 288
 Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa ggg 336
 Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly
 100 105 110
 aca atg gtc acc gtc tct tca 357
 Thr Met Val Thr Val Ser Ser
 115

<210> 38
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 38
 Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 1 5 10 15

Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr
 20 25 30

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
 35 40 45

Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln
 50 55 60

Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met
 65 70 75 80

Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly
 100 105 110

Thr Met Val Thr Val Ser Ser
 115

<210> 39
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(360)
 <223>

<400> 39
 cag gtg cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc 48
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc 96
 Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
 20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt 192
 Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
 50 55 60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac 240
 Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
 65 70 75 80

atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt 288
 Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa 336
 Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln
 100 105 110

ggg aca atg gtc acc gtc tct tca 360
 Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 40
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 40
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
 50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
 65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln
 100 105 110

Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 41
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (360)
 <223>

<400> 41
 cag gtc cag ctg gtg caa tct ggg gct gag gcg aag aag cct ggg gcc 48
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Ala Lys Lys Pro Gly Ala
 1 5 10 15

tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc 96

Ser	Val	Lys	Val	Ser	Cys	Gln	Ala	Ser	Gly	Tyr	Met	Phe	Thr	Gly	Phe	
			20				25						30			
tat	atg	cac	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggg	ctt	gag	tgg	atg	144
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
			35				40				45					
gga	tgg	atg	aac	act	aac	agt	ggt	gcc	aca	ggc	tat	gca	cac	aag	ttt	192
Gly	Trp	Met	Asn	Thr	Asn	Ser	Gly	Ala	Thr	Gly	Tyr	Ala	His	Lys	Phe	
			50				55				60					
cag	gac	agg	gtc	acc	ctg	acc	agg	gac	acg	tcc	atc	agc	aca	ggc	tac	240
Gln	Asp	Arg	Val	Thr	Leu	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Gly	Tyr	
			65				70				75				80	
atg	gag	ctg	ggc	ggc	ctg	aca	tct	gac	gac	acg	gcc	gtg	tat	tat	tgt	288
Met	Glu	Leu	Gly	Gly	Leu	Thr	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85							90				95		
gcg	aga	acc	cag	gag	gtt	tac	tac	tac	gct	atg	gac	gtc	tgg	ggc	caa	336
Ala	Arg	Thr	Gln	Glu	Val	Tyr	Tyr	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln	
			100				105						110			
ggg	acc	acg	gtc	acc	gtc	tcc	tca									360
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser									
			115				120									

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<210> 42
<211> 120
<212> PRT
<213> Homo sapiens
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<400>      42
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Ala Lys Lys Pro Gly Ala
1              5              10              15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
          20              25              30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35              40              45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
          50              55              60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
65              70              75              80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
          85              90              95

Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln
          100              105              110

Gly Thr Thr Val Thr Val Ser Ser
          115              120

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<210> 43
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (369)
 <223>

<400> 43
 cag gtc cag ctg gtg caa tct ggg gga ggc ttg gta cag cca ggg cgg 48
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 tcc ctg aga ctc tcc tgt aca act tct gga ttc acc ttt agt gat tat 96
 Ser Leu Arg Leu Ser Cys Thr Thr Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30
 gct ttg agc tgg gtc cgc cag gct cca ggg agg ggg ctg gag tgg gta 144
 Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45
 ggt ttc att aga aat aaa att tat ggt ggg aca aca gat tac gcc gca 192
 Gly Phe Ile Arg Asn Lys Ile Tyr Gly Gly Thr Thr Asp Tyr Ala Ala
 50 55 60
 tct gtg aaa ggc aga ttc acc atc tca aga gat gat tcc aaa agt atc 240
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
 65 70 75 80
 gcc tat ctg caa atg aac agc ctg aaa acc gag gac tca gcc gtc tat 288
 Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Ser Ala Val Tyr
 85 90 95
 tac tgt act aga gat tcg ggt gtg gtg act gct gcc tac ttt gac tac 336
 Tyr Cys Thr Arg Asp Ser Gly Val Val Thr Ala Ala Tyr Phe Asp Tyr
 100 105 110
 tgg ggc cag ggc acc ctg gtc acc gtc tcc tca 369
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 44
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 44
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Thr Thr Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45

Gly Phe Ile Arg Asn Lys Ile Tyr Gly Gly Thr Thr Asp Tyr Ala Ala
 50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
 65 70 75 80

Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Ser Ala Val Tyr
 85 90 95

Tyr Cys Thr Arg Asp Ser Gly Val Val Thr Ala Ala Tyr Phe Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 45
 <211> 366
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(366)
 <223>

<400> 45
 cag gtc cag ctg gtg caa tct ggg gga ggc gtg gtc cag cct ggg agg 48
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg 336
 Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp

100	105	110	
ggc cag ggg acc acg gtc acc gtc tcc tca			366
Gly Gln Gly Thr Thr Val Thr Val Ser Ser			
115	120		

<210> 46
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 46	
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn	
20 25 30	
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	
50 55 60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp	
100 105 110	
Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120	

<210> 47
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(360)
 <223>

<400> 47		
cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc		48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala		
1 5 10 15		
tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc		96
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe		
20 25 30		

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt 192
 Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
 50 55 60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac 240
 Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
 65 70 75 80

atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt 288
 Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa 336
 Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln
 100 105 110

ggg aca atg gtc acc gtc tct tca 360
 Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 48
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 48
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
 50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
 65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln
 100 105 110

Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 49

<211> 353
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(351)
 <223>

<400> 49
 cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc tca gtg 48
 Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
 1 5 10 15
 aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc tat atg 96
 Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr Met
 20 25 30
 cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga tgg 144
 His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp
 35 40 45
 atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt cag gac 192
 Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln Asp
 50 55 60
 agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac atg gag 240
 Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met Glu
 65 70 75 80
 ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt gcg aga 288
 Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95
 acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa ggg aca 336
 Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly Thr
 100 105 110
 atg gtc acc gtc tct tc 353
 Met Val Thr Val Ser
 115

<210> 50
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 50
 Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
 1 5 10 15
 Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr Met
 20 25 30
 His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp
 35 40 45

Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln Asp
 50 55 60

Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met Glu
 65 70 75 80

Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly Thr
 100 105 110

Met Val Thr Val Ser
 115

<210> 51
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(360)
 <223>

<400> 51
 cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc 48
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc 96
 Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
 20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt 192
 Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
 50 55 60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac 240
 Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
 65 70 75 80

atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt 288
 Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa 336
 Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln
 100 105 110

gga acc ctg gtc acc gtc tct tca 360

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 52
<211> 120
<212> PRT
<213> Homo sapiens

<400> 52
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe
20 25 30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe
50 55 60
Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr
65 70 75 80
Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 53
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(357)
<223>

<400> 53
gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc tca 48
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
1 5 10 15
gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc tat 96
Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr
20 25 30
atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga 144
Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
35 40 45

tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt cag 192
 Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln
 50 55 60

gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac atg 240
 Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met
 65 70 75 80

gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt gcg 288
 Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

aga acc cag gag gtt tac tac tac gct atg gac gta ctg ggg cca agg 336
 Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Leu Gly Pro Arg
 100 105 110

gac aat ggt cac cgt ctc ttc 357
 Asp Asn Gly His Arg Leu Phe
 115

<210> 54
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 54
 Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 1 5 10 15

Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr
 20 25 30

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
 35 40 45

Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln
 50 55 60

Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met
 65 70 75 80

Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Leu Gly Pro Arg
 100 105 110

Asp Asn Gly His Arg Leu Phe
 115

<210> 55
 <211> 342
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

<223>

<400> 55

gat	att	gtg	atg	acc	cag	act	cca	gac	tcc	ctg	gct	gtg	tct	ctg	ggc	48
Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly	
1				5					10					15		

gag	agg	gcc	acc	atc	aac	tgc	aag	tcc	agc	cag	agt	gtt	tta	tac	agc	96
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser	
			20					25					30			

tcc	aac	aat	aag	aac	tac	tta	gct	tgg	tac	cag	cag	aaa	cca	gga	cag	144
Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	
			35				40					45				

cct	cct	aaa	ctg	ctc	att	tac	tgg	gca	tct	acc	cgg	gaa	tcc	ggg	gtc	192
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val	
		50				55					60					

cct	gac	cga	ttc	agt	ggc	agc	ggg	tct	ggg	aca	gat	ttc	act	ctc	acc	240
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	
65					70					75					80	

atc	agc	acc	ctg	cag	gct	gaa	gat	gtg	gca	gtt	tat	tac	tgt	cag	caa	288
Ile	Ser	Thr	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	
				85					90					95		

tat	tat	agt	act	cct	ccg	acg	ttc	ggc	caa	ggg	acc	aag	gtg	gaa	atc	336
Tyr	Tyr	Ser	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	
			100					105						110		

aaa	cgt															342
Lys	Arg															

<210> 56

<211> 114

<212> PRT

<213> Homo sapiens

<400> 56

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly
1				5					10					15	

Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser
			20					25					30		

Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln
			35				40					45			

Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val
			50			55					60				

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg

<210> 57
<211> 337
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(336)
<223>

<400> 57
gat ctt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Leu Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg cac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp His Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act cct ccg acg ttc ggc caa ggg acc aaa gtg gat atc a 337
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
100 105 110

<210> 58
<211> 112
<212> PRT

<213> Homo sapiens

<400> 58

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Asp Leu Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1              5              10              15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
              20              25              30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp His Gln Gln Lys Pro Gly Gln
              35              40              45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
              50              55              60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65              70              75              80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
              85              90              95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
              100              105              110

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<210> 59

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

<223>

<400> 59

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gat att gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc      48
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1              5              10              15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc      96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
              20              25              30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag      144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
              35              40              45

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
              50              55              60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc      240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65              70              75              80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa      288

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<400> 61
gat att gtg atg act cag tct cca ctc tcc ctg ccc gtc acc cct gga 48
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ttg gat agt 96
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30

gat gat gga aac acc tat ttg gac tgg tac ctg cag aag cca ggg cag 144
 Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
 35 40 45

tct cca cag ctc cta atc tat acg ctt tcc tat cgg gcc tct gga gtc 192
 Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
 50 55 60

cca gac agg ttc agt ggc agt ggg tca ggc act gat ttc aca ctg aaa 240
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
 65 70 75 80

atc agc agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa 288
 Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
 85 90 95

cgt ata gag ttt cct tac act ttt ggc cag ggg acc aaa gtg gat atc 336
 Arg Ile Glu Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
 100 105 110

aaa cgt 342
 Lys Arg

<210> 62
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 62
 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30

Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
 35 40 45

Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
 50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
 65 70 75 80

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
 85 90 95

Arg Ile Glu Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
 100 105 110

Lys Arg

<210> 63
 <211> 342
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(342)
 <223>

<400> 63
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 Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15
 gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ttg gat agt 96
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30
 gat gat gga aac acc tat ttg gac tgg tac ctg cag aag cca ggg cag 144
 Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
 35 40 45
 tct cca cag ctc cta atc tat acg ctt tcc tat cgg gcc tct gga gtc 192
 Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
 50 55 60
 cca gac agg ttc agt ggc agt ggg tca ggc act gat ttc aca ctg aaa 240
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
 65 70 75 80
 atc agc agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa 288
 Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
 85 90 95
 cgt ata gag ttt cct tac act ttt ggc cag ggg acc aag gtg gaa atc 336
 Arg Ile Glu Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110
 aaa cgt 342
 Lys Arg

<210> 64
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 64
 Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30
 Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
 35 40 45
 Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
 65 70 75 80
 Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
 85 90 95
 Arg Ile Glu Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110
 Lys Arg

<210> 65
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(339)
 <223>

<400> 65
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 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15
 gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ttg gat agt 96
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30
 gat gat gga aac acc tat ttg gac tgg tac ctg cag aag cca ggg cag 144
 Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
 35 40 45
 tct cca cag ctc cta atc tat acg ctt tcc tat cgg gcc tct gga gtc 192
 Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
 50 55 60
 cca gac agg ttc agt ggc agt ggg tca ggc act gat ttc aca ctg aaa 240
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
 65 70 75 80
 atc agc agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa 288
 Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
 85 90 95

gct aca caa ttg tac act ttt ggc cag ggg acc aag gtg gag atc aaa 336
 Ala Thr Gln Leu Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

cgt 339
 Arg

<210> 66
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 66
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30
 Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
 35 40 45
 Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
 65 70 75 80
 Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
 85 90 95
 Ala Thr Gln Leu Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

Arg

<210> 67
 <211> 342
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(342)
 <223>

<400> 67
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 Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser

20	25	30	
tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag			144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln			
35	40	45	
cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc			192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val			
50	55	60	
cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc			240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr			
65	70	75	80
atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa			288
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln			
85	90	95	
tat tat agt act cct ccg acg ttc ggc caa ggg acc aag ctg gag atc			336
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile			
100	105	110	
aaa cgt			342
Lys Arg			

<210> 68
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 68	
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1	15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20	30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35	45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50	60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65	80
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85	95
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile	
100	110
Lys Arg	

<210> 69
 <211> 342
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(342)
 <223>

<400> 69
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 Asp Val Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta cac aag 96
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Lys
 20 25 30
 tcc aac aat aag aac tat tta gct tgg tac cag cag aaa cca gga cag 144
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 cct cct aaa ttg ctc att cac tgg gct tct acc cgg gaa ttc ggg gtc 192
 Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
 50 55 60
 cct gac cga ctc agt ggc agc ggg tct gcg aca gat ttc act ctc acc 240
 Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
 65 70 75 80
 atc agc agc ctg cag gct gaa gac gtg gca gtc tat tac tgt cag caa 288
 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 tat tat gct gtt cct ctc acc ttc ggc caa ggg aca cga ctg gag att 336
 Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
 100 105 110
 aaa cgt 342
 Lys Arg

<210> 70
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 70
 Asp Val Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Lys
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
 50 55 60

Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
 100 105 110

Lys Arg

<210> 71
 <211> 342
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(342)
 <223>

<400> 71
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 Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
 Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 tat tat agt act cct ccg acg ttc agc caa ggg acc aag gtg gaa atc 336
 Tyr Tyr Ser Thr Pro Pro Thr Phe Ser Gln Gly Thr Lys Val Glu Ile
 100 105 110

aaa cgt
Lys Arg

342

<210> 72
<211> 114
<212> PRT
<213> Homo sapiens

<400> 72
Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Tyr Tyr Ser Thr Pro Pro Thr Phe Ser Gln Gly Thr Lys Val Glu Ile
100 105 110
Lys Arg

<210> 73
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(342)
<223>

<400> 73
gat gtt gtg atg act cag tct cca gac tcc ctg act gtg tct ctg ggc 48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly
1 5 10 15
gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30
tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144

Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln		
	35						40					45					
cct	cct	aag	ctg	ctc	att	tac	tgg	gca	cct	acc	cgg	gaa	tcc	ggg	gtc	192	
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Pro	Thr	Arg	Glu	Ser	Gly	Val		
	50					55					60						
cct	gac	cga	ttc	agt	ggc	agc	ggg	tct	ggg	aca	gat	ttc	act	ctc	acc	240	
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr		
65					70				75					80			
atc	agc	agc	ctg	cag	gct	gaa	gat	gtg	gca	gtt	tat	tac	tgt	cag	caa	288	
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln		
			85					90						95			
tat	tat	agt	act	cct	ccg	acg	ttc	ggc	cag	ggg	acc	aag	gtg	gaa	atc	336	
Tyr	Tyr	Ser	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile		
		100						105					110				
aaa	cgt															342	
Lys	Arg																

<210> 74
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400>	74																
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1			5					10						15			
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser		
		20					25					30					
Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln		
	35						40					45					
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Pro	Thr	Arg	Glu	Ser	Gly	Val		
	50				55						60						
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr		
65				70					75					80			
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln		
			85					90						95			
Tyr	Tyr	Ser	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile		
		100						105					110				
Lys	Arg																

<210> 75
 <211> 342

<212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(342)
 <223>

<400> 75
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 Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 gag agg gcc acc atc aac tgc aag tcc agc cag ggt gtt tta cac aag 96
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Gly Val Leu His Lys
 20 25 30
 tcc aac aat aag aac tat tta gct tgg tac cag cag aaa cca gga cag 144
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 cct cct aaa ttg ctc att cac tgg gct tct acc cgg gaa ttc ggg gtc 192
 Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
 50 55 60
 cct gac cga ctc agt ggc agc ggg tct gcg aca gat ttc act ctc acc 240
 Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
 65 70 75 80
 atc agc agc ctg cag gct gaa gac gtg gca gtc tat tac tgt cag caa 288
 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 tat tat gct gtt cct ctc acc ttc ggc caa ggg aca cga ctg gag att 336
 Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
 100 105 110
 aaa cgt 342
 Lys Arg

<210> 76
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 76
 Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Gly Val Leu His Lys
 20 25 30
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
 50 55 60

Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
 100 105 110

Lys Arg

<210> 77
 <211> 342
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(342)
 <223>

<400> 77

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Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly	
1 5 10 15	
gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20 25 30	
tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35 40 45	
cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc	192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50 55 60	
cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc	240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65 70 75 80	
atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa	288
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85 90 95	
tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa atc	336
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
100 105 110	
aaa cgt	342
Lys Arg	

<210> 78
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 78

Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110
 Lys Arg

<210> 79
 <211> 342
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (342)

<223>

<400> 79

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 Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Pro Leu Gly
 1 5 10 15
 gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta cac aag 96
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Lys
 20 25 30
 tcc aac aat aag aac cat tta gct tgg tac cag cag aaa cca gga cag 144
 Ser Asn Asn Lys Asn His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

cct cct aaa ttg ctc att cac tgg gct tct acc cgg gaa ttc ggg gtc 192
Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
50 55 60

cct gac cga ctc agt ggc agc ggg tct gcg aca gat ttc act ctc acc 240
Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
65 70 75 80

atc aac agc ctg cag gct gaa gac gcg gca gtc tat tac tgt cag caa 288
Ile Asn Ser Leu Gln Ala Glu Asp Ala Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat	tat	gct	gtt	cct	ctc	acc	ttc	ggc	caa	ggg	aca	cga	ctg	gag	att	336
Tyr	Tyr	Ala	Val	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	
		100						105				110				

aaa cgt		342
Lys Arg	.	

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<210> 80
<211> 114
<212> PRT
<213> Homo sapiens
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<400> 80
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Pro Leu Gly
1          5          10          15
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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Lys
20 25 30

Ser Asn Asn Lys Asn His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
50 55 60

Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Asn Ser Leu Gln Ala Glu Asp Ala Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

Lys Arg

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<210> 81
<211> 342
<212> DNA
<213> Homo sapiens
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<220>

<221> CDS

<222> (1)..(342)

<223>

<400> 81

gat	att	gtg	atg	act	cag	tct	cca	gac	tcc	ctg	gct	gtg	tct	ctg	ggc	48
Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly	
1				5					10					15		

gag	agg	gcc	acc	atc	aac	tgc	aag	tcc	agc	cag	agt	gtt	tta	tac	agc	96
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser	
			20					25					30			

tcc	aac	aat	aag	aac	tac	tta	gct	tgg	tac	cag	cag	aaa	cca	gga	cag	144
Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	
			35				40					45				

cct	cct	aaa	ctg	ctc	att	tac	tgg	gca	tct	acc	cgg	gaa	tcc	ggg	gtc	192
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val	
		50				55					60					

cct	gac	cga	ttc	agt	ggc	agc	ggg	tct	ggg	aca	gat	ttc	act	ctc	acc	240
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	
65					70					75				80		

atc	agc	acc	ctg	cag	gct	gaa	gat	gtg	gca	gtt	tat	tac	tgt	cag	caa	288
Ile	Ser	Thr	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	
				85					90					95		

tat	tat	agt	act	cct	ccg	acg	ttc	ggc	caa	ggg	acc	aaa	gtg	gat	atc	336
Tyr	Tyr	Ser	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Asp	Ile	
			100					105					110			

aaa	cgt															342
Lys	Arg															

<210> 82

<211> 114

<212> PRT

<213> Homo sapiens

<400> 82

Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly
1				5					10					15	

Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser
			20					25					30		

Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln
			35				40					45			

Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val
			50			55					60				

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
100 105 110

Lys Arg

<210> 83
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(342)
<223>

<400> 83
gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aaa ttg ctc att cac tgg gct tct acc cgg gaa ttc ggg gtc 192
Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
50 55 60

cct gac cga ctc agt ggc agc ggg tct gcg aca gat ttc act ctc acc 240
Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gac gtg gca gtc tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat gct gtt cct ctc acc ttc ggc caa ggg aca cga ctg gag att 336
Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

aaa cgt 342
Lys Arg

<210> 84
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 84
 Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val
 50 55 60
 Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
 100 105 110
 Lys Arg

<210> 85
 <211> 342
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(342)
 <223>

<400> 85
 gac atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
 Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
 Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa atc 336
 Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110

aaa cgt 342
 Lys Arg

<210> 86
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 86
 Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110
 Lys Arg

<210> 87
 <211> 327
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(327)

<223>

<400> 87

gaa att gtg ctg act cag tct cca ggc acc ctg tct ttg tct cca ggg 48
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

gaa aga gcc acc ctc tcc tgc aag gcc agt cag agt ttt agc agc aac 96
 Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Phe Ser Ser Asn
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctg ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt aaa tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt acc tca ccg 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Thr Ser Pro
 85 90 95

tac act ttt ggc ctg ggg acc aag gtg gag atc aaa cgt 327
 Tyr Thr Phe Gly Leu Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 88

<211> 109

<212> PRT

<213> Homo sapiens

<400> 88

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Phe Ser Ser Asn
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Thr Ser Pro
 85 90 95

Tyr Thr Phe Gly Leu Gly Thr Lys Val Glu Ile Lys Arg

100

105

<210> 89
 <211> 325
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (324)
 <223>

<400> 89
 gat gtt ggg atg aca cag tct tca gcc acc cta tct ttg tct cca ggg 48
 Asp Val Gly Met Thr Gln Ser Ser Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agg att agc agt tat 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr
 20 25 30
 tta gcc tgg tac caa cag aaa cct ggc cag gct ccc aga ctc ctc atc 144
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 tat gag gca gtc aaa agg gcc act ggc atc cca gcc agg ttc agt ggc 192
 Tyr Glu Ala Val Lys Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 agt ggg tct ggg aca gag ttc acc ctc acc atc aac agc cta gag cct 240
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro
 65 70 75 80
 gaa gat ttt gca gtt tat ttc tgt cag cag cgt ggc agc tgt cct ggg 288
 Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Arg Gly Ser Cys Pro Gly
 85 90 95
 acg ttc ggc cag ggg acc aag ctg gag atc aaa cgt t 325
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

<210> 90
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 90
 Asp Val Gly Met Thr Gln Ser Ser Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Glu Ala Val Lys Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Arg Gly Ser Cys Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 91
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(366)
<223>

<400> 91
cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc acc ggc tac 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

gga tgg atc aac cct aac agt ggt ggc aca aag tat gca cag aag ttt 192
Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe
50 55 60

cag ggc agg gtc acc atg acc agg gac acg tcc atc agc aca gcc tac 240
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

atg gag ctg agc agg ctg aga tct gac gac acg gcc gtg tat tac tgt 288
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga gga tac gat att ttg act ggt tat ggc tgg ttc gac ccc tgg 336
Ala Arg Gly Tyr Asp Ile Leu Thr Gly Tyr Gly Trp Phe Asp Pro Trp
100 105 110

ggc cag gga acc ctg gtc acc gtc tcc tca 366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 92
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 92
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
 20 25 30
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Tyr Asp Ile Leu Thr Gly Tyr Gly Trp Phe Asp Pro Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 93
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(360)
 <223>

<400> 93
 cag gtc cag ctg gtg caa tct ggg gga ggc ttg gtc cag cct ggg ggg 48
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agt agc tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 tgg atg agt tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtg 144
 Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gcc aac ata aag caa gat gga agt gag aaa tac tat gtg gac tct gtg 192
 Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val

50	55	60	
aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat			240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr			
65	70	75	80
ctg caa atg aac acc ctg aga gcc gag gac acg gct gtg tat tac tgt			288
Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
	85	90	95
gcg aga gat cgt ttg tgg acc cag ggg ttt ttt gac tac tgg ggc cag			336
Ala Arg Asp Arg Leu Trp Thr Gln Gly Phe Phe Asp Tyr Trp Gly Gln			
	100	105	110
gga acc ctg gtc acc gtc tcc tca			360
Gly Thr Leu Val Thr Val Ser Ser			
	115	120	

<210> 94
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 94	
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
20	30
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35	45
Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val	
50	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr	
65	80
Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85	95
Ala Arg Asp Arg Leu Trp Thr Gln Gly Phe Phe Asp Tyr Trp Gly Gln	
100	110
Gly Thr Leu Val Thr Val Ser Ser	
115	120

<210> 95
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (1) .. (339)

<223>

<400> 95

gac atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc	48
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1 5 10 15	
gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20 25 30	
tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35 40 45	
cct cct aac ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc	192
Pro Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50 55 60	
cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc	240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65 70 75 80	
atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa	288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85 90 95	
tat tat act act ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc	336
Tyr Tyr Thr Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
100 105 110	
aaa	339
Lys	

<210> 96

<211> 113

<212> PRT

<213> Homo sapiens

<400> 96

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1 5 10 15	
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20 25 30	
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35 40 45	
Pro Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50 55 60	
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65 70 75 80	

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

Tyr Tyr Thr Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110

Lys

<210> 97
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 97
 caggtkcagc tgggtgcagtc tgg 23

<210> 98
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 98
 caggtccagc ttgtgcagtc tgg 23

<210> 99
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 99
 saggtccagc tgggtacagtc tgg 23

<210> 100
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 100
 caratgcagc tgggtgcagtc tgg 23

<210> 101
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 101
 cagatcacct tgaaggagtc tggc 24

<210> 102
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 102
 caggtcacct tgarggagtc tggc 24

<210> 103
 <211> 23
 <212> DNA
 <213> Artificial

<220>
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<400> 103
 gargtgcagc tgggtggagtc tgg 23

<210> 104
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 104
 caggtgcagc tgggtggagtc tgg 23

<210> 105
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 105
gaggtgcagc tggtggagtc tgg 23

<210> 106
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 106
cagstgcagc tgcaggagtc gggc 24

<210> 107
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 107
caggtgcagc tacagcagtg gggc 24

<210> 108
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 108
gargtgcagc tggtgcagtc tgga 24

<210> 109
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 109
caggtacagc tgcagcagtc aggt 24

<210> 110
<211> 23
<212> DNA
<213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

 <400> 110
 caggtscagc tggtgcaatc tgg 23

 <210> 111
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 111
 tgaggagacg gtgaccaggg tkcc 24

 <210> 112
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 112
 tgaagagacg gtgaccattg tccc 24

 <210> 113
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 113
 tgaggagacg gtgaccgtgg tccc 24

 <210> 114
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 114
 racatccaga tgaccagtc tcca 24

 <210> 115

<211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 115
 gmcattccagt tgaccacagtc tcca 24

<210> 116
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 116
 gccattccrga tgaccacagtc tcca 24

<210> 117
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 117
 gtcattctgga tgaccacagtc tcca 24

<210> 118
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 118
 gatattgtga tgaccacagac tcca 24

<210> 119
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 119
 gatrttgtga tgactcagtc tcca 24

<210> 120
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 120
 gaaattgtgt tgacrcagtc tcca 24

<210> 121
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 121
 gaaatagtga tgacgcagtc tcca 24

<210> 122
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 122
 gaaattgtaa tgacacagtc tcca 24

<210> 123
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 123
 gacatcgtga tgaccagtc tcca 24

<210> 124
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 124
gaaacgacac tcacgcagtc tcca 24

<210> 125
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 125
gaaattgtgc tgactcagtc tcca 24

<210> 126
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 126
gatgttgatga tgacacagtc tcca 24

<210> 127
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 127
acgtttgatt tccaccttgg tccc 24

<210> 128
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 128
acgtttgatc tccaccttgg tccc 24

<210> 129
<211> 24
<212> DNA
<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 129

acgttttgata tccacttttg tccc

24

<210> 130

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 130

acgtttaatc tccagtcgtg tccc

24

<210> 131

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 131

cagtctgtgc tgactcagcc accc

24

<210> 132

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 132

cagtctgtgy tgacgcagcc gcc

24

<210> 133

<211> 22

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 133

cagtctgccc tgactcagcc ts

22

<210> 134

<211> 24
 <212> DNA
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<220>
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<400> 134
 tcctatgwgC tgactcagcc accc 24

<210> 135
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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<400> 135
 tcctatgagc tgacacagcy accc 24

<210> 136
 <211> 24
 <212> DNA
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<220>
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<400> 136
 tcttctgagc tgactcagga ccct 24

<210> 137
 <211> 24
 <212> DNA
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<220>
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<400> 137
 tcctatgagc tgatgcagcc accc 24

<210> 138
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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<400> 138
 cagcctgtgc tgactcaatc atcc 24

<210> 139
 <211> 24
 <212> DNA
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<220>
 <223> Artificially Synthesized Primer Sequence

<400> 139
 cagcttgtagc tgactcaatc gccg 24

<210> 140
 <211> 24
 <212> DNA
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<220>
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<400> 140
 ctgcctgtgc tgactcagcc cccg 24

<210> 141
 <211> 24
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<220>
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<400> 141
 cagcctgtgc tgactcagcc ayct 24

<210> 142
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 142
 caggctgtgc tgactcagcc ggct 24

<210> 143
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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<400> 143
aatatttatgc tgactcagcc ccac 24

<210> 144
<211> 24
<212> DNA
<213> Artificial

<220>
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<400> 144
cagrctgtgg tgactcagga gccc 24

<210> 145
<211> 24
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<220>
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<400> 145
cagactgtgg tgacccagga gcca 24

<210> 146
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<220>
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<400> 146
cwgcctgtgc tgactcagcc acct 24

<210> 147
<211> 24
<212> DNA
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<220>
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<400> 147
caggcagggc tgactcagcc accc 24

<210> 148
<211> 24
<212> DNA
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<220>
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 <400> 148
 acctaggacg gtgaccttgg tccc 24

 <210> 149
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 149
 acctaggacg gtcagcttgg tccc 24

 <210> 150
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
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 <400> 150
 accgaggacg gtcagctggg tgcc 24

 <210> 151
 <211> 91
 <212> DNA
 <213> Artificial

 <220>
 <223> Template Linker Sequence

 <400> 151
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 gcggatcgga catccagatg acccagtctc c 91

 <210> 152
 <211> 28
 <212> DNA
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 <220>
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 <400> 152
 gcaccctggg caccgtctcc tcaggtgg 28

<210> 153
 <211> 28
 <212> DNA
 <213> Artificial

<220>
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<400> 153
 ggacaatggt caccgtctct tcaggtgg 28

<210> 154
 <211> 28
 <212> DNA
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<220>
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<400> 154
 gaaccctggt caccgtctcc tcaggtgg 28

<210> 155
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 155
 ggaccacggt caccgtctcc tcaggtgg 28

<210> 156
 <211> 32
 <212> DNA
 <213> Artificial

<220>
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<400> 156
 ggagactggg tcactctggat gtccgatccg cc 32

<210> 157
 <211> 32
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 157
ggagactgag tcatcacaac atccgatccg cc 32

<210> 158
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 158
ggagactgcg tcaacacaat ttccgatccg cc 32

<210> 159
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 159
ggagactggg tcatcacgat gtccgatccg cc 32

<210> 160
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 160
ggagactgcg tgagtgtcgt ttccgatccg cc 32

<210> 161
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 161
ggagactgag tcagcacaat ttccgatccg cc 32

<210> 162
<211> 42
<212> DNA
<213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 162
 ggcggctgcg tcaacacaga ctgcatccg ccaccgccag ag 42

<210> 163
 <211> 42
 <212> DNA
 <213> Artificial

<220>
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<400> 163
 gcaggctgag tcagagcaga ctgcatccg ccaccgccag ag 42

<210> 164
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 164
 ggtggctgag tcagcacata ggacatccg ccaccgccag ag 42

<210> 165
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 165
 gggtcctgag tcagctcaga agacatccg ccaccgccag ag 42

<210> 166
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 166
 ggcgggttgag tcagtataac gtgcatccg ccaccgccag ag 42

<210> 167
 <211> 42

<212> DNA
 <213> Artificial

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 167
 gacggctgag tcagcacaga ctgcgatccg ccaccgccag ag 42

 <210> 168
 <211> 42
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 <220>
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 <400> 168
 tggggctgag tcagcataaa attcgatccg ccaccgccag ag 42

 <210> 169
 <211> 39
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 <220>
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 <400> 169
 agtattgacc atggcccagg tgcagctggt gcagtctgg 39

 <210> 170
 <211> 39
 <212> DNA
 <213> Artificial

 <220>
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 <400> 170
 agtattgacc atggcccagg tcaacttaag ggagtctgg 39

 <210> 171
 <211> 39
 <212> DNA
 <213> Artificial

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 171
 agtattgacc atggccgagg tgcagctggt ggagtctgg 39

<210> 172
 <211> 39
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 <213> Artificial

<220>
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<400> 172
 agtattgacc atggcccagg tgcagctgca ggagtcggg 39

<210> 173
 <211> 39
 <212> DNA
 <213> Artificial

<220>
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<400> 173
 agtattgacc atggcccagg tgcagctggt gcagctctgc 39

<210> 174
 <211> 39
 <212> DNA
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<220>
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<400> 174
 agtattgacc atggcccagg tacagctgca gcagtcagg 39

<210> 175
 <211> 34
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 175
 taatgaattc acgtttgatt tccaccttgg tccc 34

<210> 176
 <211> 34
 <212> DNA
 <213> Artificial

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 176
taatgaattc acgtttgatc tccagcttgg tccc 34

<210> 177
<211> 34
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 177
taatgaattc acgtttgata tccactttgg tccc 34

<210> 178
<211> 34
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 178
taatgaattc acgtttgatc tccaccttgg tccc 34

<210> 179
<211> 34
<212> DNA
<213> Artificial

<220>
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<400> 179
taatgaattc acgtttaatc tccagtcgtg tccc 34

<210> 180
<211> 34
<212> DNA
<213> Artificial

<220>
<223> Artificially Synthesized Primer Sequence

<400> 180
taatgaattc acctaggacg gtgaccttgg tccc 34

<210> 181
<211> 34
<212> DNA
<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 181

taatgaattc acctaggacg gtcagcttgg tccc

34

<210> 182

<211> 34

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 182

taatgaattc acctaaaacg gtgagctggg tccc

34

<210> 183

<211> 861

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (861)

<223>

<400> 183

atg aaa tac ctg ctg ccg acc gct gct gct ggt ctg ctg ctc ctc gct
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
 1 5 10 15

48

gcc cag ccg gcg atg gcc atg gcc cag gtg cag ctg gtg cag tct ggg
 Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly
 20 25 30

96

gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct
 Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
 35 40 45

144

tct gga tac acc ttc acc ggc tac tat atg cac tgg gtg cga cag gcc
 Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala
 50 55 60

192

cct gga caa ggg ctt gag tgg atg gga tgg atc aac cct aac agt ggt
 Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly
 65 70 75 80

240

ggc aca aag tat gca cag aag ttt cag ggc agg gtc acc atg acc agg
 Gly Thr Lys Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg
 85 90 95

288

gac acg tcc atc agc aca gcc tac atg gag ctg agc agg ctg aga tct
 Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser
 100 105 110

336

gac gac acg gcc gtg tat tac tgt gcg aga gga tac gat att ttg act 384
 Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Asp Ile Leu Thr
 115 120 125

ggc tat ggc tgg ttc gac ccc tgg ggc cag gga acc ctg gtc acc gtc 432
 Gly Tyr Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
 130 135 140

tcc tca ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga 480
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160

tcg gac atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg 528
 Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
 165 170 175

ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac 576
 Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr
 180 185 190

agc tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga 624
 Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
 195 200 205

cag cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg 672
 Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
 210 215 220

gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc 720
 Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 225 230 235 240

acc atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag 768
 Thr Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
 245 250 255

caa tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa 816
 Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
 260 265 270

atc aaa cgt cgt gaa ttc gac tac aag gat gac gac gat aag tga 861
 Ile Lys Arg Arg Glu Phe Asp Tyr Lys Asp Asp Asp Asp Lys
 275 280 285

<210> 184

<211> 286

<212> PRT

<213> Homo sapiens

<400> 184

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly
 20 25 30

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
 35 40 45
 Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala
 50 55 60
 Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly
 65 70 75 80
 Gly Thr Lys Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg
 85 90 95
 Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser
 100 105 110
 Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Asp Ile Leu Thr
 115 120 125
 Gly Tyr Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
 130 135 140
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160
 Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
 165 170 175
 Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr
 180 185 190
 Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
 195 200 205
 Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
 210 215 220
 Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 225 230 235 240
 Thr Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
 245 250 255
 Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
 260 265 270
 Ile Lys Arg Arg Glu Phe Asp Tyr Lys Asp Asp Asp Asp Lys
 275 280 285

<210> 185
 <211> 846
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (1) .. (846)

<223>

<400> 185

atg aaa tac ctg ctg ccg acc gct gct gct ggt ctg ctg ctc ctc gct	48
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala	
1 5 10 15	
gcc cag ccg gcg atg gcc atg gcc cag gtg cag ctg gtg cag tct ggg	96
Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly	
20 25 30	
gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct	144
Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala	
35 40 45	
tct gga tac acc ttc acc ggc tac tat atg cac tgg gtg cga cag gcc	192
Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala	
50 55 60	
cct gga caa ggg ctt gag tgg atg gga tgg atc aac cct aac agt ggt	240
Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly	
65 70 75 80	
ggc aca aag tat gca cag aag ttt cag ggc agg gtc acc atg acc agg	288
Gly Thr Lys Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg	
85 90 95	
gac acg tcc atc agc aca gcc tac atg gag ctg agc agg ctg aga tct	336
Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser	
100 105 110	
gac gac acg gcc gtg tat tac tgt gcg aga gga tac gat att ttg act	384
Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Asp Ile Leu Thr	
115 120 125	
ggc tat ggc tgg ttc gac ccc tgg ggc cag gga acc ctg gtc acc gtc	432
Gly Tyr Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val	
130 135 140	
tcc tca ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga	480
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
145 150 155 160	
tcg gaa att gtg ctg act cag tct cca ggc acc ctg tct ttg tct cca	528
Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro	
165 170 175	
ggg gaa aga gcc acc ctc tcc tgc aag gcc agt cag agt ttt agc agc	576
Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Phe Ser Ser	
180 185 190	
aac tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctg	624
Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu	
195 200 205	
ctc atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc	672

Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe
 210 215 220

agt ggc agt aaa tct ggg aca gac ttc act ctc acc atc agc aga ctg 720
 Ser Gly Ser Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu
 225 230 235 240

gag cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt acc tca 768
 Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Thr Ser
 245 250 255

ccg tac act ttt ggc cag ggg acc aag gtg gag atc aaa cgt cgt gaa 816
 Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Arg Glu
 260 265 270

ttc gac tac aag gat gac gac gat aag tga 846
 Phe Asp Tyr Lys Asp Asp Asp Asp Lys
 275 280

<210> 186
 <211> 281
 <212> PRT
 <213> Homo sapiens

<400> 186
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly
 20 25 30

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
 35 40 45

Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala
 50 55 60

Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly
 65 70 75 80

Gly Thr Lys Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg
 85 90 95

Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser
 100 105 110

Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Asp Ile Leu Thr
 115 120 125

Gly Tyr Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
 130 135 140

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160

Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro

165								170				175			
Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gln	Ser	Phe	Ser	Ser
180								185				190			
Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu
195								200				205			
Leu	Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe
210								215				220			
Ser	Gly	Ser	Lys	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu
225				230				235				240			
Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Val	Thr	Ser
				245				250				255			
Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Arg	Glu
				260				265				270			
Phe	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys							
275				280											

<210> 187
 <211> 852
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(852)
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<400>	187	
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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala		
1 5 10 15		
gcc cag ccg gcg atg gcc atg gcc cag gtc cag ctg gtg caa tct ggg		96
Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly		
20 25 30		
gga ggc ttg gtc cag cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc		144
Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala		
35 40 45		
tct gga ttc acc ttt agt agc tat tgg atg agt tgg gtc cgc cag gct		192
Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg Gln Ala		
50 55 60		
cca ggg aag ggg ctg gag tgg gtg gcc aac ata aag caa gat gga agt		240
Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile Lys Gln Asp Gly Ser		
65 70 75 80		
gag aaa tac tat gtg gac tct gtg aag ggc cga ttc acc atc tcc aga		288
Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg		

85 ,										90					95					
gac	aac	gcc	aag	aac	tca	ctg	tat	ctg	caa	atg	aac	acc	ctg	aga	gcc					336
Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Thr	Leu	Arg	Ala					
			100						105					110						
gag	gac	acg	gct	gtg	tat	tac	tgt	gcg	aga	gat	cgt	ttg	tgg	acc	cag					384
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Leu	Trp	Thr	Gln					
			115					120					125							
ggg	ttt	ttt	gac	tac	tgg	ggc	cag	gga	acc	ctg	gtc	acc	gtc	tcc	tca					432
Gly	Phe	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser					
			130				135					140								
ggg	ggg	ggg	ggg	tcg	ggg	ggg	ggg	ggg	tcg	ggg	ggg	ggc	gga	tcg	gac					480
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Ser	Asp				
					150				155						160					
atc	gtg	atg	acc	cag	tct	cca	gac	tcc	ctg	gct	gtg	tct	ctg	ggc	gag					528
Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly	Glu					
				165					170					175						
agg	gcc	acc	atc	aac	tgc	aag	tcc	agc	cag	agt	gtt	tta	tac	agc	tcc					576
Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser	Ser					
			180					185					190							
aac	aat	aag	aac	tac	tta	gct	tgg	tac	cag	cag	aaa	cca	gga	cag	cct					624
Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro					
			195				200					205								
cct	aac	ctg	ctc	att	tac	tgg	gca	tct	acc	cgg	gaa	tcc	ggg	gtc	cct					672
Pro	Asn	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val	Pro					
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gac	cga	ttc	agt	ggc	agc	ggg	tct	ggg	aca	gat	ttc	act	ctc	acc	atc					720
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile					
					230				235					240						
agc	agc	ctg	cag	gct	gaa	gat	gtg	gca	gtt	tat	tac	tgt	cag	caa	tat					768
Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr					
				245				250					255							
tat	act	act	ccg	tgg	acg	ttc	ggc	caa	ggg	acc	aag	gtg	gaa	atc	aaa					816
Tyr	Thr	Thr	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			260				265						270							
cgt	gaa	ttc	gac	tac	aag	gat	gac	gac	gat	aag	tga									852
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 35 40 45
 Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg Gln Ala
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 Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile Lys Gln Asp Gly Ser
 65 70 75 80
 Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
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 Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala
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 Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Trp Thr Gln
 115 120 125
 Gly Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 130 135 140
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
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 Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu
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 Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser
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 Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro
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 Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro
 210 215 220
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 225 230 235 240
 Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr
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 Tyr Thr Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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 Arg Glu Phe Asp Tyr Lys Asp Asp Asp Asp Lys
 275 280